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- 11 -

Kasibhatla *et al.* Appl. No. 10/826,909

Remarks

Upon entry of the foregoing amendment, claims 1-46 are pending in the application, with claims 1, 14, 32, 34, 38, 40, 41 and 44 being the independent claims. Applicants have amended claim 31 to make it dependent on claim 14. Support for the amendment to claim 31 may be found, *inter alia*, in Example 39. These changes are believed to introduce no new matter, and their entry is respectfully requested.

Election

The Examiner requested an election of an invention directed to one of the following of Groups I-DXCI. Groups CCLXXXI-CCCVI, corresponding to claims 14-15 and 19-30 and newly amended claim 31, are drawn to a method of identifying potentially therapeutic anticancer compounds comprising contacting one Transferrin Receptor Related Apoptosis Inducing Protein with test compounds, wherein compounds that bind one Transferrin Receptor Related Apoptosis Inducing Protein are potentially therapeutic anticancer compound. The Examiner has requested an election of one Transferrin Receptor Related Apoptosis Inducing Protein, corresponding to one of SEQ ID NOS:1-26.

Applicants hereby provisionally elect to prosecute the invention of Group CCLXXXI, represented by claims 14-15 and 19-30 and newly amended claim 31. Applicants further elect SEQ ID NO:1 and the species 1-(3-methyl-2-butenyl)-3,3-dimethyl-1,3,3a,4,5,12a-hexahydro-7,13-dioxo-1,5-methano-furo[3,4-d]xanthene of

claim 31. This election is made without prejudice to or disclaimer of the other claims or inventions disclosed.

This election is made with traverse.

Applicants respectfully request rejoinder of groups CCLXXXI-CCCVI. While the Examiner has required election of one of SEQ ID NOS:1-26 for prosecution, Applicants respectfully point out to the Examiner that SEQ ID NOS:1-26 are related sequences. Applicants attach herewith sequence alignments of SEQ ID NO:1 and SEQ ID NOS:2-26 generated by BLAST (Basic Local Alignment Search Tool). As seen from the alignments, SEQ ID NOS:1, 2, 3 and 8 are identical sequences. Further, there is only one amino acid difference between SEQ ID NO:1 and SEQ ID NOS:4, 5, 6, 9 and 10. Further, SEQ ID NOS:11-21 are fragments of 639 or 640 amino acids in length and have one or three amino acid differences (greater than 99% identical) compared with the corresponding fragments in SEQ ID NO:1. Therefore, at a minimum, Applicants request that the Examiner rejoin Groups CCLXXXII-CCLXXXVI and CCLXXXVIII-CCXC (corresponding to SEQ ID NOS:2-6 and SEQ ID NOS:8-10) with Group CCLXXXI, because the sequences are identical or differ by only one amino acid and would therefore involve the same search. Likewise, Groups CCXCI-CCCI (corresponding to SEQ ID NOS:11-21) should be rejoined with Group CCLXXXI on the same basis. SEQ ID NOS:7 and 22-26 are smaller fragments of 15-63 amino acids and share from 81-100% identity with the corresponding fragments of SEQ ID NO:1. Therefore, a search of SEQ ID NO:1 would necessarily be coextensive with a search for these sequences as well and

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Applicants respectfully request rejoinder of Groups CCLXXXVII and CCCII-CCCVI

with Group CCLXXXI.

Reconsideration and withdrawal of the Restriction Requirement, and

consideration and allowance of all pending claims, are respectfully requested. It is not

believed that extensions of time are required, beyond those that may otherwise be

provided for in accompanying documents. However, if additional extensions of time are

necessary to prevent abandonment of this application, then such extensions of time are

hereby petitioned under 37 C.F.R. § 1.136(a), and any fees required therefor are hereby

authorized to be charged to our Deposit Account No. 19-0036.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

Robert W. Esmond

Attorney for Applicants Registration No. 32,893

Date:

Not. 20, 2006

1100 New York Avenue, N.W. Washington, D.C. 20005-3934 (202) 371-2600

599905_1.DOC



Entrez

BLAST

OMIM

Taxonomy

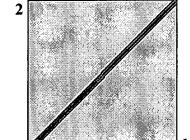
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1	
Masking character option X for protein, n for nucleotide Masking color option Black	
Show CDS translation Align	

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $gi|6164848|gb|AAF04564.1|AF187320_1$ transferrin receptor [Homo sapiens] >gi|108935939|sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 (TfR1) (TR) (TfR) (CD71 antigen) (T9) (p90) >gi|12654697|gb|AAH01188.1| TFRC protein [Homo sapiens] >gi|94717625|gb|ABF47088.1| transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



```
Score = 1531 bits (3964), Expect = 0.0
 Identities = 760/760 (100%), Positives = 760/760 (100%), Gaps = 0/760 (0%)
            MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
Query
            MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
Sbjct
      1
            MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
                                                                           60
            {\tt RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR}
                                                                           120
Query
       61
            RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
            {\tt RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR}
                                                                           120
Sbjct
      61
       121 RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
                                                                           180
            RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
      121 RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 180
Sbjct
```

```
VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
                                                                           240
      181
Query
            VWRDOHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
           VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
                                                                           240
      181
Sbjct
           KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                           300
Query
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
           KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                           300
Sbjct
      301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
                                                                           360
Query
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
          AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
                                                                           360
Sbjct
      301
           STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Query
      361
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
      361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                           420
Sbjct
           VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           480
Query
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
      421 VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           480
Sbjct
          YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                           540
Query
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
       481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                           540
Sbjct
      541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                           600
Query
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                           600
Sbict
                                                                           660
      601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Query
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
           LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
                                                                           660
Sbjct
       601
           GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
                                                                           720
Query
       661
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
           GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct
       661
           QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
       721
Query
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
           QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct
```

```
CPU time: 0.04 user secs. 0.02 sys. secs 0.06 total secs.
```

```
Lambda K H 0.318 0.135 0.399
```

Gapped Lambda K H 0.267 0.0410 0.140

```
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 4468
Number of extensions: 2537
Number of successful extensions: 1
Number of sequences better than 10.0: 1
```

Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,435,209,301
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,435,209,158
Effective search space: 885524050486
Effective search space used: 885524050486
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.0000 wordsize: 3 Filter View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: gi|12654697|gb|AAH01188.1|TFRC protein [Homo sapiens]
>gi|108935939|sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr)
(CD71 antigen) (T9) (p90) >gi|6164848|gb|AAF04564.1|AF187320_1 transferrin receptor [Homo sapiens] >gi|94717625|gb|ABF47088.1| transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 1531 bits (3964),Expect = 0.0Identities = 760/760 (100%), Positives = 760/760 (100%), Gaps = 0/760 (0%) SEQIANO MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK 60 Query 1 ${\tt MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK}$ 60 Sbjct ${\tt MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK}$ ${\tt RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR}$ 120 Query RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR ${\tt RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR}$ 120 Sbjct 61 ${\tt 121} \quad {\tt RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK}$ 180 Query RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 121 RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK Sbjct

```
VWRDOHFVKIOVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
                                                                          240
Query
            VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
       181 VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
                                                                          240
Sbjct
      241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                          300
Query
            \verb"KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH"
       241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                          300
Sbjct
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Query
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
      301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
                                                                          360
Sbjct
       361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                          420
Query
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
      361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                          420
Sbjct
      421 VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           480
Query
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
      421 VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                          480
Sbjct
       481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                          540
Query
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       481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbict
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Query
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                          600
Sbjct
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                           660
Query
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
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                                                                          660
Sbjct
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
       GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Query
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct
       661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
       721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                      760
Query
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
      721 ONNGAFNETLFRNOLALATWTIQGAANALSGDVWDIDNEF
                                                      760
Sbict
```

```
0.04 total secs.
                                  0.01 sys. secs
CPU time:
             0.03 user secs.
```

Lambda K 0.318 0.135 0.399

Gapped

Lambda K H

0.0410 0.267 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1 Number of Hits to DB: 4468 Number of extensions: 2537

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Page 3 of 3

Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Entrez

BLAST

OMIM

Taxonomy

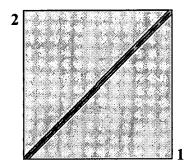
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1	
x_dropoff: 50 expect: 10.000 wordsize: 3 <u>Filter</u> ✓ View option Standard	
Masking character option X for protein, n for nucleotide Masking color option Black	
☐ Show CDS translation Align	

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $gi|4507457|ref|NP_003225.1|$ transferrin receptor [Homo sapiens] >gi|37433|emb|CAA25527.1| unnamed protein product [Homo sapiens] >gi|339516|gb|AAA61153.1| transferrin receptor >gi|224192|prf||1011297A transferrin receptor Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 1529 bits (3958),Expect = 0.0Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%)SEQTONO MMDOARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK Query MMDOARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK Sbjct MMDOARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK 1 120 RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR Query RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR 120 Sbjct 61 $\verb"RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK"$ 180 Query RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK Sbjct RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 180 121 VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK Query

Page 2 of 3 منت آ

```
VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
            VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
                                                                           240
Sbjct
       181
           KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                           300
Query
       241
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
           KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                           300
Sbjct
       241
       301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
                                                                           360
Query
            AHLGTGDPYTPGFPSFNHTOFPPSRSSGLPNIPVOTISRAAAEKLFGNMEGDCPSDWKTD
          AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
                                                                           360
Sbjct
       301
       361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                           420
Query
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                           420
Sbjct
       361
                                                                           480
           VGTALLLKLAOMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
       421
Query
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
       421 VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           480
Sbjct
           YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Query
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
       481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                           540
Sbjct
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Query
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                           600
Sbjct
                                                                           660
Query
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
            LTHDVELNLDYERYNSOLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
                                                                           660
Sbjct
           GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
                                                                           720
Query
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
           GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct
       661
Query
           QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                       760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
       721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct
                                   0.01 sys. secs
                                                           0.05 total secs.
CPU time:
              0.04 user secs.
Lambda
           K
                  Н
   0.318
           0.135
                     0.399
Gapped
Lambda
           K
   0.267
           0.0410
                     0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 4451
Number of extensions: 2525
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
```

Page 3 of 3

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399 Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits) X2: 129 (49.7 bits) X3: 129 (49.7 bits) S1: 41 (21.7 bits) S2: 83 (36.6 bits)



Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix
BLOSUM62
gap open:
11
gap extension:
1

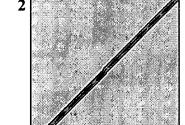
x_dropoff:
50
expect:
10.000
wordsize:
3
Filter
✓ View option
Standard

Masking character option
X for protein, n for nucleotide
Masking color option
Black

Show CDS translation
Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: gi|37433|emb|CAA25527.1|unnamed protein product [Homo sapiens] >gi|4507457|ref|NP_003225.1| transferrin receptor [Homo sapiens] >gi|339516|gb|AAA61153.1| transferrin receptor >gi|224192|prf||1011297A transferrin receptor Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 1529 bits (3958), Expect = 0.0Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%) SCOIDNO! MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK Query MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK Sbjct 120 Query RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR 120 Sbjct 61 RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 180 Query RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 121 RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 180 Sbjct Ouery VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK

```
VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
           VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
                                                                           240
Sbjct
       181
           {\tt KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH}
                                                                           300
Query
       241
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
           KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                           300
Sbjct
       241
                                                                           360
          AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
Query
            AHLGTGDPYTPGFPSFNHTOFPPSRSSGLPNIPVOTISRAAAEKLFGNMEGDCPSDWKTD
          AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
                                                                           360
Sbjct
       301
       361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                           420
Query
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
       361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                           420
Sbjct
          VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           480
Query
       421
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
       421 VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           480
Sbjct
           YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
       481
Query
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
       481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                           540
Sbjct
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                           600
Query
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                           600
Sbjct
                                                                           660
Query
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
                                                                           660
Sbjct
           GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
                                                                           720
Query
       661
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
           GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct
       661
Query
           QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                      760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
       721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                      760
Sbjct
```

```
CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.
```

Lambda K H

0.318 0.135 0.399

Gapped

Lambda K H

0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1 Number of Hits to DB: 4451

Number of extensions: 2525

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399 Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits) X2: 129 (49.7 bits) X3: 129 (49.7 bits) S1: 41 (21.7 bits)

S2: 83 (36.6 bits)





Entrez

BLAST

MIMO

Taxonomy

Structure

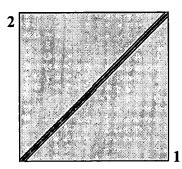
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1	
x_dropoff: 50 expect: 10.000 wordsize: 3 <u>Filter</u> ✓ View option Standard	
Masking character option X for protein, n for nucleotide Masking color option Black	
Show CDS translation Align	

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: gi|339516|gb|AAA61153.1|transferrin receptor >gi|4507457|ref|NP_003225.1| transferrin receptor [Homo sapiens] >gi|37433|emb|CAA25527.1| unnamed protein product [Homo sapiens] >gi|224192|prf||1011297A transferrin receptor Length = 760 (1 .. 760)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



```
Score = 1529 \text{ bits } (3958),
                             Expect = 0.0
 Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%)
            {\tt MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK}
Query
            MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
            MMDOARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
Sbjct
      1
            RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
Query
       61
            {\tt RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR}
            {\tt RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR}
                                                                             120
Sbjct
       61
       121 RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
                                                                             180
            RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
       121 RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
                                                                             180
Sbjct
       181 VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
```



Sbjct	181	VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK	240
Query	241	KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH	300
Sbjct	241	KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH	300
Query	301	AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD	360
Sbjct	301	AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD	360
Query	361	STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG	420
Sbjct	361	STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG	420
Query	421	VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT	480
Sbjct	421	VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT	480
Query	481	YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA	540
Sbjct	481	YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA	540
Query	541	AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK	600
Sbjct	541	AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK	600
Query	601	LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF	660 660
Sbjct	601	LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK	720
Query	661	GNAEKTDRFVMKKLNDRVMRVEIHFLSPIVSPKESPFRHVFWGSGSHTLPALLENLKLRK GNAEKTDRFVMKKLNDRVMRVEIHFLSPIVSPKESPFRHVFWGSGSHTLPALLENLKLRK GNAEKTDRFVMKKLNDRVMRVEIHFLSPIVSPKESPFRHVFWGSGSHTLPALLENLKLRK	720
Sbjct	661	QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760	720
Query	721 721	QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760	
Sbjct	/21	MUNGWINE I DI KUMTUMINI I I MANUMUNINGON AND INNEE 100	

```
CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.
```

Lambda K H 0.318 0.135 0.399

Gapped

Lambda K H

0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1 Number of Hits to DB: 4451 Number of extensions: 2525

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1



Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399 Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits) X2: 129 (49.7 bits) X3: 129 (49.7 bits) S1: 41 (21.7 bits) S2: 83 (36.6 bits)



Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

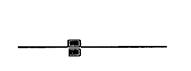
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ✓ View option Standard

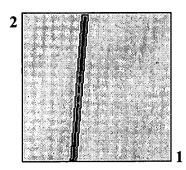
Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: gi|1336700|gb|AAB35972.1|transferrin receptor; TfR [Cavia] >gi|2144140|pir||S68317 transferrin receptor - guinea pig (fragment) Length = 63 (1 .. 63)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



```
Score = 118 bits (295), Expect = 2e-24
Identities = 54/63 (85%), Positives = 57/63 (90%), Gaps = 0/63 (0%)
```

Query 261 KITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHAHLGTGDPYTPGFPSFNHTQ 320
KITFAEKVANAESLNA+GVLIY+D TKFPI A+L FGH HLGTGDPYTPGFPSFNHTQ

Sbjct 1 KITFAEKVANAESLNALGVLIYLDWTKFPIPKADLPVFGHVHLGTGDPYTPGFPSFNHTQ 60

Query 321 FPP 323 FPP Sbjct 61 FPP 63

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H

```
0.318
           0.135
                     0.399
Gapped
Lambda
           K
           0.0410
                     0.140
   0.267
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 413
Number of extensions: 242
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```



Entrez

BLAST

OMIM

Taxonomy

Structure

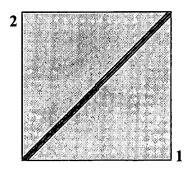
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1	
x_dropoff: 50 expect: 10.000 wordsize: 3 <u>Filter</u> ✓ View option Standard	
Masking character option X for protein, n for nucleotide Masking color option Black	
Show CDS translation Align	

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $gi|108935939|sp|P02786|TFR1_HUMAN$ Transferrin receptor protein 1 (TfR1) (TR) (Trfr) (CD71 antigen) (T9) (p90) >gi|6164848|gb|AAF04564.1|AF187320_1 transferrin receptor [Homo sapiens] >gi|12654697|gb|AAH01188.1| TFRC protein [Homo sapiens] >gi|94717625|gb|ABF47088.1| transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Expect = 0.0Score = 1531 bits (3964),Identities = 760/760 (100%), Positives = 760/760 (100%), Gaps = 0/760 (0%)Satono MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK 60 Query MMDOARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK 60 Sbjct 1 MMDOARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR 120 Query 61 RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR 120 Sbjct 61 180 121 RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK Query RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 121 RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK Sbjct

```
VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
                                                                           240
Query
       181
            VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
           VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
                                                                           240
Sbjct
       181
           KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                           300
       241
Query
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
           KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                           300
Sbjct
       241
       301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
Query
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
Sbjct
       301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
                                                                           360
       361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Query
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
       361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                           420
Sbjct
           VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           480
Query
       421
            VGTALLLKLAQMFSDMVLKDGFQPSRS11FASWSAGDFGSVGATEWLEGYLSSLHLKAFT
       421 VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           480
Sbjct
                                                                           540
       481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Query
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
       481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct
                                                                           600
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Ouery
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                           600
Sbjct
                                                                           660
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Query
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
          LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
                                                                           660
       601
Sbjct
           GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
       661
                                                                           720
Query
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
           {\tt GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK}
                                                                           720
Sbjct
       661
       721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Query
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                      760
      721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
```

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda K H

0.318 0.135 0.399

Gapped

Lambda K H

0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1 Number of Hits to DB: 4468 Number of extensions: 2537

Number of successful extensions: 1 Number of sequences better than 10.0: 1 Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Entrez

BLAST

MIMO

Taxonomy

Structure

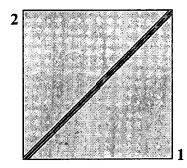
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gar	p open: 11 gap extension: 1	
	0.000 wordsize: 3 Filter ✓ View option Standard	
Masking character option	X for protein, n for nucleotide Masking color option Black	
☐ Show CDS translation	Align	

Sequence 1: lcl|1_seq_1 Length = 2249 (1 .. 2249)

Sequence 2: lcl|2_seq_2 Length = 2249 (1 .. 2249)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Cakana

			2 bits (8171), Expect = 0.0	
	Ident	ities	= 2246/2249 (99%), Positives = 2246/2249 (99%), Gaps = 0/2249	(0%)
SEQIDA	30			
l	Query	1	METMETASPGLNALAARGSERALAPHESERASNLEUPHEXXXXXXXXXPRLEUSERTYRT	60
_			METMETASPGLNALAARGSERALAPHESERASNLEUPHEGLYGLYGLUPRLEUSERTYRT	
9	Sbjct	1	METMETASPGLNALAARGSERALAPHESERASNLEUPHEGLYGLYGLUPRLEUSERTYRT	60
	_		WELL CONTROLLED TO A RECENT AS A DOLLAR ORDER OF THE OWN OF THE OWN OF THE OWN OF THE OWN	120
	Query	61	HRARGPHESERLEUALAARGGLNVALASPGLYASPASNSERHISVALGLUMETXXXXXXX	120
	_		HRARGPHESERLEUALAARGGLNVALASPGLYASPASNSERHISVALGLUMETLYSLEUA	
	Sbjct	61	HRARGPHESERLEUALAARGGLNVALASPGLYASPASNSERHISVALGLUMETLYSLEUA	120
	Query	121	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTHRLYSALAASNVALTHRLYSPRLYSAR	180
			LAVALASPGLUGLUGLUASNALAASPASNASNTHRLYSALAASNVALTHRLYSPRLYSAR	
	Sbjct	121	LAVALASPGLUGLUGLUASNALAASPASNASNTHRLYSALAASNVALTHRLYSPRLYSAR	180
	Query	181	GCYSSERGLYSERILECYSTYRGLYTHRXXXXXXXXXXXXXXXXXXXXXXXXXXXXYPH	240
	_		GCYSSERGLYSERILECYSTYRGLYTHRILEALAVALILEVALPHEPHELEUILEGLYPH	
	Sbjct	181	GCYSSERGLYSERILECYSTYRGLYTHRILEALAVALILEVALPHEPHELEUILEGLYPH	240
	_			

Query	241	EMETILEGLYTYRLEUGLYTYRCYSLYSGLYVALGLUPRLYSTHRGLUCYSXXXXXXXX EMETILEGLYTYRLEUGLYTYRCYSLYSGLYVALGLUPRLYSTHRGLUCYSGLUARGLEU	300
Sbjct	241	EMETILEGLYTYRLEUGLYTYRCYSLYSGLYVALGLUPRLYSTHRGLUCYSGLUARGLEU	300
Query	301	XXXXXYTHRGLUSEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	360
Sbjct	301	ALAGLYTHRGLUSERPRVALARGGLUGLUPRGLYGLUASPPHEPRALAALAARGARGLEU	360
Query	361	TYRTRPASPASPLEULYSARGLYSLEUSERGLULYSLEUASPSERTHRASPPHETHRGLY TYRTRPASPASPLEULYSARGLYSLEUSERGLULYSLEUASPSERTHRASPPHETHR	420
Sbjct	361	TYRTRPASPASPLEULYSARGLYSLEUSERGLULYSLEUASPSERTHRASPPHETHRSER	420
Query	421	THRIXXXXXXXXXXASNGLUASNSERTYXXXXXXXXXXXXXXXXXYSERGLNLYSASPG THRILELYSLEULEUASNGLUASNSERTYRVALPRARGGLUALAGLYSERGLNLYSASPG	480
Sbjct	421	THRILELYSLEULEUASNGLUASNSERTYRVALPRARGGLUALAGLYSERGLNLYSASPG	480
Query	481	LUASNXXXXXXXXTYRVALGLUASNGLNPHEARGGLUPHELYSLEUSERLYSVALTRPA	540
Sbjct	481	LUASNLEUALALEUTYRVALGLUASNGLNPHEARGGLUPHELYSLEUSERLYSVALTRPA	540
Query	541	RGASPGLNHISPHEVALLYSILEGLNVALLYSASPSERALAGLNASNSERXXXXXXXXX RGASPGLNHISPHEVALLYSILEGLNVALLYSASPSERALAGLNASNSERVALILEILEV	600
Sbjct	541	RGASPGLNHISPHEVALLYSILEGLNVALLYSASPSERALAGLNASNSERVALILEILEV	600
Query	601	XXXSPLYSASNGLYARGLEUVALTYRLEUVALGLUASNPRGLYGLYTYRVALALATYRSE ALASPLYSASNGLYARGLEUVALTYRLEUVALGLUASNPRGLYGLYTYRVALALATYRSE	660
Sbjct	601	ALASPLYSASNGLYARGLEUVALTYRLEUVALGLUASNPRGLYGLYTYRVALALATYRSE	660
Query	661	RLYSALAALATHRVALTHRGLYLYSLEUVALHISALAASNPHEGLYTHRLYSLYSASPPH RLYSALAALATHRVALTHRGLYLYSLEUVALHISALAASNPHEGLYTHRLYSLYSASPPH	720
Sbjct	661	RLYSALAALATHRVALTHRGLYLYSLEUVALHISALAASNPHEGLYTHRLYSLYSASPPH	720
Query	721	EGLUASPLEUTYRTHRPRVALASNGLYSERXXXXXXXXXXXXXXXXXXXXXXXXILETHR EGLUASPLEUTYRTHRPRVALASNGLYSERILEVALILEVALARGALAGLYLYSILETHR	780
Sbjct	721	EGLUASPLEUTYRTHRPRVALASNGLYSERILEVALILEVALARGALAGLYLYSILETHR	780
Query	781	PHEXXXXXXXXXXXXXXXXXXXXXXXXERLEUASNALAILEGLYVALLEUILETYRMET PHEALAGLULYSVALALAASNALAGLUSERLEUASNALAILEGLYVALLEUILETYRMET	840
Sbjct	781	PHEALAGLULYSVALALAASNALAGLUSERLEUASNALAILEGLYVALLEUILETYRMET	840
Query	841	ASPGLNTHRLYSPHEPRILEVXXXXXXXXXXXXEUSERPHEPHEGLYHISALAHISLEUG ASPGLNTHRLYSPHEPRILEVALASNALAGLULEUSERPHEPHEGLYHISALAHISLEUG	900
Sbjct	841	ASPGLNTHRLYSPHEPRILEVALASNALAGLULEUSERPHEPHEGLYHISALAHISLEUG	900
Query	901	LYTHRGLYASPPRTYRTHRPRGLYPHEPRSERPHEASNHISTHRGLNPHXXXXXXXXXX LYTHRGLYASPPRTYRTHRPRGLYPHEPRSERPHEASNHISTHRGLNPHEPRPRSERARG	960
Sbjct	901	LYTHRGLYASPPRTYRTHRPRGLYPHEPRSERPHEASNHISTHRGLNPHEPRPRSERARG	960
Query	961	XXXXXXXLYLEUPRASNILEPRVALGLNTHRILESEXXXXXXXXXXXXXXXXXYSLEUPH SERSERGLYLEUPRASNILEPRVALGLNTHRILESERARGALAALAALAGLULYSLEUPH	1020
Sbjct	961	SERSERGLYLEUPRASNILEPRVALGLNTHRILESERARGALAALAGLULYSLEUPH	1020
Query	1021	EGLYASNMETGLUGLYASPCYSPRSERASPTRPLYSTHRASPSERTHRCYSARGMETVAL EGLYASNMETGLUGLYASPCYSPRSERASPTRPLYSTHRASPSERTHRCYSARGMETVAL	1080
Sbjct	1021	EGLYASNMETGLUGLYASPCYSPRSERASPTRPLYSTHRASPSERTHRCYSARGMETVAL	1080
Query	1081	THRSERGLUSERLYSASNVALLYSLEUTHRVALSERASNVAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	1140
Sbjct	1081	THRSERGLUSERLYSASNVALLYSLEUTHRVALSERASNVALLEULYSGLUILELYSILE	1140

Query	1141	XXUASNILEPHEGLYVALILELYSGLYPHEVALGLUPRASPHISTYRXXXXXXXXXXXX LEUASNILEPHEGLYVALILELYSGLYPHEVALGLUPRASPHISTYRVALVALVALGLYA	1200
Sbjct	1141	LEUASNILEPHEGLYVALILELYSGLYPHEVALGLUPRASPHISTYRVALVALVALGLYA	1200
Query	1201	XXXXXXXXSPALATRPGLYPRGXXXXXXXXXSSERGLYVALGLYTHRXXXXXXXXXX LAGLNARGASPALATRPGLYPRGLYALAALALYSSERGLYVALGLYTHRALALEULEULE	1260
Sbjct	1201	LAGLNARGASPALATRPGLYPRGLYALAALALYSSERGLYVALGLYTHRALALEULEULE	1260
Query	1261	XXXXXXXXXXXNMETPHESERASPMETVALLEULYSASPGLYPHEGLNPRSERARGSER ULYSLEUALAGLNMETPHESERASPMETVALLEULYSASPGLYPHEGLNPRSERARGSER	1320
Sbjct	1261	ULYSLEUALAGLNMETPHESERASPMETVALLEULYSASPGLYPHEGLNPRSERARGSER	1320
Query	1321	ILEILEPHEALASERTRPSERALAGLYASPPHEGLYSERVALGLYALATHRGLUTRPLEU ILEILEPHEALASERTRPSERALAGLYASPPHEGLYSERVALGLYALATHRGLUTRPLEU	1380
Sbjct	1321	ILEILEPHEALASERTRPSERALAGLYASPPHEGLYSERVALGLYALATHRGLUTRPLEU	1380
Query	1381	GLUGLYTYXXXXXXXXXXXXXXXXXXXXXYSALAPHETHRTYRILEASNLEUASPLYSALA GLUGLYTYRLEUSERSERLEUHISLEULYSALAPHETHRTYRILEASNLEUASPLYSALA	1440
Sbjct	1381	GLUGLYTYRLEUSERSERLEUHISLEULYSALAPHETHRTYRILEASNLEUASPLYSALA	1440
Query	1441	VALLEUGLYTHRSERASNPHELYSVALSERALASERPRLEULEUTYRTHRLEUILEGLUL VALLEUGLYTHRSERASNPHELYSVALSERALASERPRLEULEUTYRTHRLEUILEGLUL	1500
Sbjct	1441	VALLEUGLYTHRSERASNPHELYSVALSERALASERPRLEULEUTYRTHRLEUILEGLUL	1500
Query	1501	YSTHRMETGLNASNVALLYSHISPRVALTHRGLYGLNPHELEUTYRGLNASPSERASNTR YSTHRMETGLNASNVALLYSHISPRVALTHRGLYGLNPHELEUTYRGLNASPSERASNTR	1560
Sbjct	1501	YSTHRMETGLNASNVALLYSHISPRVALTHRGLYGLNPHELEUTYRGLNASPSERASNTR	1560
Query	1561	PALASERLYSVALGLULYSLEUTHRLEXXXXXXXXXXXXXXHEPRPHELEUALATYRSER PALASERLYSVALGLULYSLEUTHRLEUASPASNALAALAPHEPRPHELEUALATYRSER	1620
Sbjct	1561	PALASERLYSVALGLULYSLEUTHRLEUASPASNALAALAPHEPRPHELEUALATYRSER	1620
Query	1621	GLYILEPRALAVALSERPHECYSPHECYSGLUASPTHRASPTYRPRTYRLEUGLYTHRTH GLYILEPRALAVALSERPHECYSPHECYSGLUASPTHRASPTYRPRTYRLEUGLYTHRTH	1680
Sbjct	1621	GLYILEPRALAVALSERPHECYSPHECYSGLUASPTHRASPTYRPRTYRLEUGLYTHRTH	1680
Query	1681	RMETASPTHRTYRLYSXXXXXXXXXXXUARGILEPRGLULEUASNLYSVXXXXXXXXXXX RMETASPTHRTYRLYSGLULEUILEGLUARGILEPRGLULEUASNLYSVALALAARGALA	1740
Sbjct	1681	RMETASPTHRTYRLYSGLULEUILEGLUARGILEPRGLULEUASNLYSVALALAARGALA	1740
Query	1741	XXXXXXXXXXXXXXXXXXNPHEVALILELYSLEUTHRHISASPVALGLULEUASNLEU ALAALAGLUVALALAGLYGLNPHEVALILELYSLEUTHRHISASPVALGLULEUASNLEU	1800
Sbjct	1741	ALAALAGLUVALALAGLYGLNPHEVALILELYSLEUTHRHISASPVALGLULEUASNLEU	1800
Query	1801	ASPTYRGLUARGTYRASNSERGLNLEULEUSERPHEVALARGASPLEUASNGLNTYRARG ASPTYRGLUARGTYRASNSERGLNLEULEUSERPHEVALARGASPLEUASNGLNTYRARG	1860
Sbjct	1801	ASPTYRGLUARGTYRASNSERGLNLEULEUSERPHEVALARGASPLEUASNGLNTYRARG	1860
Query	1861	ALAASPILELYSGLUMETGLYLEUSERLEUGLNTRPLEUTYRSERALAARGGLYASPPHE ALAASPILELYSGLUMETGLYLEUSERLEUGLNTRPLEUTYRSERALAARGGLYASPPHE	1920
Sbjct	1861	ALAASPILELYSGLUMETGLYLEUSERLEUGLNTRPLEUTYRSERALAARGGLYASPPHE	1920
Query	1921	PHEARGALATHRSERARGLEUTHRTHRASPPHEGLYASNALAGLULYSTHRASPARGPHE PHEARGALATHRSERARGLEUTHRTHRASPPHEGLYASNALAGLULYSTHRASPARGPHE	1980
Sbjct	1921	PHEARGALATHRSERARGLEUTHRTHRASPPHEGLYASNALAGLULYSTHRASPARGPHE	1980
Query	1981	VALMETLYSLYSLEUASNASPARGVALMETARGVALGLUTYRHISPHELEUSERPRTYRV VALMETLYSLYSLEUASNASPARGVALMETARGVALGLUTYRHISPHELEUSERPRTYRV	2040
Sbjct	1981	VALMETLYSLYSLEUASNASPARGVALMETARGVALGLUTYRHISPHELEUSERPRTYRV	2040

Query	2041	ALSERPRLYSGLUSERPRPHEARGHISVALPHETRPGLYSERGLYSERHISTHXXXXXXX	2100
		ALSERPRLYSGLUSERPRPHEARGHISVALPHETRPGLYSERGLYSERHISTHRLEUPRA	
Sbjct	2041	ALSERPRLYSGLUSERPRPHEARGHISVALPHETRPGLYSERGLYSERHISTHRLEUPRA	2100
Query	2101	XXXXXXXGLUASNLEULYSLEUARGLYSGLNASNASNGLYALAPHEASNGLUTHRLEUP	2160
		LALEULEUGLUASNLEULYSLEUARGLYSGLNASNASNGLYALAPHEASNGLUTHRLEUP	
Sbjct	2101	LALEULEUGLUASNLEULYSLEUARGLYSGLNASNASNGLYALAPHEASNGLUTHRLEUP	2160
-			
Query	2161	HEARGASNGLNXXXXXXXXXXXXTHRTRPTHRIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	2220
E1		HEARGASNGLNLEUALALEUALATHRTRPTHRILEGLNGLYALAALAASNALALEUSERG	
Sbjct	2161	HEARGASNGLNLEUALALEUALATHRTRPTHRILEGLNGLYALAALAASNALALEUSERG	2220
	2101		
Query	2221	LYASPVALTRPASPILEASPASNGLUPHE 2249	
Query	2221		
		LYASPVALTRPASPILEASPASNGLUPHE	
Sbjct	2221	LYASPVALTRPASPILEASPASNGLUPHE 2249	

CPU time: 0.05 user secs. 0.01 sys. secs 0.06 total secs.

Lambda K H

0.314 0.130 0.376

Gapped

Lambda K H

0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 94,211

Number of extensions: 37877

Number of successful extensions: 747

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 2249

Length of database: 1,435,209,301

Length adjustment: 151

Effective length of query: 2098

Effective length of database: 1,435,209,150

Effective search space: 3011068796700

Effective search space used: 3011068796700

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 129 (49.7 bits) X3: 129 (49.7 bits)

75. 125 (15., E1C)

S1: 42 (22.0 bits)

S2: 88 (38.5 bits)





Entrez

BLAST

OMIM

Taxonomy

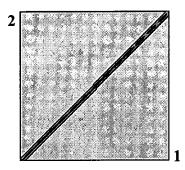
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1	
x_dropoff: 50 expect: 10.000 wordsize: 3 <u>Filter</u> ✓ View option Standard	
Masking character option X for protein, n for nucleotide Masking color option Black	
Show CDS translation Align	

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2 Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



```
Score = 1529 \text{ bits } (3958),
                                     Expect = 0.0
         Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%)
SERIDNO
                    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
        Query
                    MMDOARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
  10
        Sbjct
                    {\tt MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK}
               1
                    RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
                                                                                    120
        Query
                    RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
        Sbjct
                    RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
               61
                                                                                    180
                    RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
        Query
               121
                    RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
                                                                                    180
        Sbjct
                    RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
               121
                    VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
                                                                                    240
        Query
                    VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
        Sbjct
               181 VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
```

```
KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                           300
       241
Query
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
           KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
                                                                           300
Sbjct
       241
       301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
                                                                           360
Query
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
          AHLGTGDPYTPGFPSFNHTOFPPSRSSGLPNIPVOTISRAAAEKLFGNMEGDCPSDWKTD
                                                                           360
Sbjct
       301
       361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                           420
Query
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
           STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                           420
Sbjct
       361
       421
           VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Query
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
       421 VGTALLLKLAOMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           480
Sbjct
           YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                           540
Query
       481
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
       481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                           540
Sbjct
                                                                           600
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Query
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                           600
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbict
                                                                           660
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Query
            LTHDVELNLDYERYNSOLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct
       661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
                                                                           720
Query
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
            {\tt GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK}
                                                                           720
Sbjct
       661
       721 ONNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Query
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
       721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct
                                                           0.03 total secs.
CPU time:
              0.03 user secs.
                                   0.00 sys. secs
Lambda
           K
           0.135
                     0.399
   0.318
Gapped
Lambda
           0.0410
   0.267
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 4451
Number of extensions: 2525
Number of successful extensions: 1
```

Number of sequences better than 10.0: 1

Number of HSP's successfully gapped: 1

Length of database: 1,433,654,390

Number of HSP's gapped: 1

Length of query: 760

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399 Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.7 bits)

S2: 83 (36.6 bits)



Entrez

BLAST

MIMO

Taxonomy

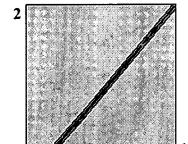
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1	
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ✓ View option Standard	
Masking character option X for protein, n for nucleotide Masking color option Black	
☐ Show CDS translation Align	

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2 Length = 640 (1 .. 640)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

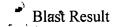


			86 bits (3327), Expect = 0.0	
	Ident:	ities	= 639/640 (99%), Positives $= 639/640 (99%)$, Gaps $= 0/640 (0%)$	
XXIDNO				
(Query	121	RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	180
			RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	
()	Sbjct	1	RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	60
	Query	181	VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK	240
			VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK	
	Sbjct	61	VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK	120
	Query	241	KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH	300
			KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH	
	Sbjct	121	KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH	180
	Query	301	AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD	360
			AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD	
	Sbjct	181	AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD	240

Page 2 of 3

```
361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                           420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
       {\tt 241} \quad {\tt STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG}
                                                                           300
Sbjct
       421 VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           480
Query
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
       301 VGTALLLKLAOMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                           360
Sbjct
       481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Query
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                           420
Sbjct
       361 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Query
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
       421 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                           480
Sbjct
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
                                                                           660
Query
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
       481 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
                                                                           540
Sbjct
       661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
                                                                           720
Query
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
       541 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK 600
Sbjct
       721 ONNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Query
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                       640
       601 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct
                                                           0.03 total secs.
                                   0.00 sys. secs
CPU time:
              0.03 user secs.
Lambda
           K
          0.135
                     0.399
   0.318
Gapped
Lambda
   0.267
           0.0410
                     0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3743
Number of extensions: 2118
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

X3: 64 (24.7 bits) S1: 41 (21.7 bits) S2: 83 (36.6 bits)





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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ✓ View option Standard

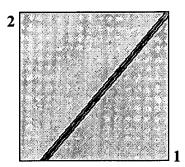
Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $|c||seq_2$ Length = 640 (1 .. 640)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



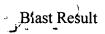
Score = 1286 bits (3327),Expect = 0.0Identities = 639/640 (99%), Positives = 639/640 (99%), Gaps = 0/640 (0%) SEQIDNO 121 RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 60 12 Sbjct 1 RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 181 VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK Query VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK Sbjct 61 VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 120 $\verb|KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH|$ 300 Query KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 180 Sbjct 121 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 360 Query 301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD 240 Sbjct 181 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD

Page 2 of 3

```
STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                          420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                          300
Sbjct
      241 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
      421 VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                          480
Query
           VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
      301 VGTALLLKLAOMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                          360
Sbjct
      481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                          540
Query
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                          420
       361 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                          600
Query
           AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
       421 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                          480
Sbjct
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
                                                                          660
Query
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
      481 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
                                                                          540
Sbjct
       GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Query
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
      541 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK 600
Sbjct
       721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Query
            ONNGAFNETLFRNOLALATWTIOGAANALSGDVWDIDNEF
       601 ONNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct
                                   0.01 sys. secs
                                                          0.04 total secs.
CPU time:
             0.03 user secs.
Lambda
          K
         0.135
                    0.399
   0.318
Gapped
Lambda
          K
                 Η
                     0.140
   0.267
          0.0410
```

```
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3743
Number of extensions: 2118
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

X3: 64 (24.7 bits) S1: 41 (21.7 bits) S2: 83 (36.6 bits)



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ✓ View option Standard

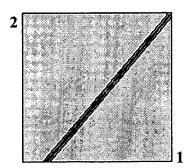
Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: |c|| seq_2 Length = 640 (1 .. 640)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1286 bits (3327), Expect = 0.0**SEQIDNO** Identities = 639/640 (99%), Positives = 639/640 (99%), Gaps = 0/640 (0%)121 RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 13 Sbjct 1 181 VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240 Query VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK Sbjct 61 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300 Query KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 121 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 180 Sbjct 301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD 360 Query AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD 240 181 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD Sbjct

```
361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                          420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
       241 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
                                                                          300
Sbjct
      421 VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                          480
Query
            VGTALLLKLAOMFSDMVLKDGFOPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
       301 VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
                                                                          360
Sbjct
       481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Query
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
       361 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
                                                                          420
Sbjct
       541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                          600
Query
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
       421 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
                                                                          480
Sbjct
                                                                          660
       601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Query
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
      481 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct
       661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
                                                                          720
Query
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
       541 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK 600
Sbjct
Query
       721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
            ONNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                      640
Sbict
       601 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                  0.01 sys. secs
                                                          0.04 total secs.
CPU time:
              0.03 user secs.
Lambda
          K
          0.135
   0.318
                    0.399
Gapped
Lambda
           K
   0.267
           0.0410
                     0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3743
Number of extensions: 2118
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
```

Effective length of database: 1,433,654,247

Effective search space: 884564670399
Effective search space used: 884564670399

Length adjustment: 143

X1: 16 (7.3 bits) X2: 38 (14.6 bits)

Effective length of query: 617

Neighboring words threshold: 9



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ✓ View option Standard

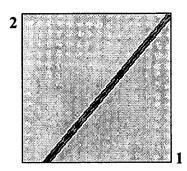
Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $|c||seq_2$ Length = 639 (1 .. 639)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 1281 bits (3314),Expect = 0.0SECTION of Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%) 122 LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV 60 LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV Sbjct 1 Query 182 WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK Sbjct 61 WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK 120 301 Query 242 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 180 Sbjct 121 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 361 Query 302 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS 181 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS 240 Sbjct

```
TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                           421
Query
      362
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
           {\tt TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV}
                                                                           300
Sbjct
       241
      422 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                           481
Query
           GTALLLKLAOMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
           {\tt GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY}
                                                                           360
       301
Sbjct
       482 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Query
            {\tt INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA}
       361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
                                                                           420
Sbjct
       542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Query
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
       421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                           480
Sbjct
       602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                           661
Query
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
       481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                           540
Sbjct
       662 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Query
           NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
       541 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ 600
Sbict
       722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Query
            NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
       601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                     639
Sbjct
                                                           0.04 total secs.
                                    0.01 sys. secs
CPU time:
              0.03 user secs.
Lambda
          K
          0.135
                     0.399
   0.318
Gapped
Lambda
           K
   0.267
           0.0410
                     0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
```



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix
BLOSUM62
gap open:
11
gap extension:
1

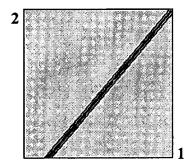
x_dropoff:
15
expect:
10.000
wordsize:
3
Filter
✓ View option
Standard

Masking character option
X for protein, n for nucleotide
Masking color option
Black

Show CDS translation
Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $|c||seq_2|$ Length = 639 (1 .. 639)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 1281 bits (3314),Expect = 0.0Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%) SECTINO 181 LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV $\verb|LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV|$ Sbjct 1 182 WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK Query WRDOHFVKIOVKDSAONSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK Sbjct WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK 61 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 301 Query DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA Sbjct DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 180 121 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS 361 Query HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS Sbjct 181 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS 240

Blast Result Page 2 of 3

```
Query 362 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                          421
           TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
       241 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                         300
Sbjct
Query 422 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
           GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
      301 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                         360
Sbjct
      482 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Query
           {\tt INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA}
      361 INLDKAVLGTSNFKVSASPLLYTLIEKTMONVKHPVTGOFLYODSNWASKVEKLTLDNAA
Sbict
      542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                          601
Query
           FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
      421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                         480
Sbjct
      602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                          661
Query
           THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct 481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
      662 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
                                                                         721
Query
           NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct 541 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ 600
      722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Query
           NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct
      601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                    639
                                                          0.05 total secs.
CPU time: 0.04 user secs.
                                   0.01 sys. secs
Lambda
          K H
  0.318 0.135
                    0.399
Gapped
Lambda
          K
                 Η
  0.267
          0.0410
                    0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```



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Structure

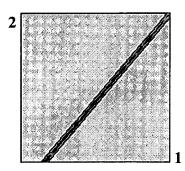
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1	
x_dropoff: 15 expect: 10.000 wordsize: 3 <u>Filter</u> ✓	View option Standard
Masking character option X for protein, n for nucleotide	Masking color option Black
Show CDS translation Align	

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $|c||seq_2$ Length = 639 (1 .. 639)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
Expect = 0.0
         Score = 1281 \text{ bits } (3314),
\mathcal{S}QTDN0 Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)
               122 LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV
                    LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
   16
                                                                                    60
                    LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV
        Sbjct
        Query
               182
                   WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
                    WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
        Sbjct
               61
                    WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
                                                                                    120
                                                                                    301
        Query
                    DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
                    DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
               121 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
                                                                                    180
        Sbjct
                                                                                    361
               302 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
        Query
                    HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
               181 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
                                                                                    240
        Sbjct
```

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```
362 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                         421
Query
           TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
Sbjct
      241 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                         300
      422 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                         481
Query
           GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
      301 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                         360
Sbjct
      482 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Query
           INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
      361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA 420
Sbjct
      542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Query
           FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
      421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                         480
Sbjct
      602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                         661
Query
           THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
     481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                         540
Sbjct
      662 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Query
           NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
     541 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ 600
Sbjct
      722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Query
           NNGAFNETLFRNOLALATWTIOGAANALSGDVWDIDNEF
Sbjct 601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                    639
```

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda K H

0.318 0.135 0.399

Gapped

Lambda K H

0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1 Number of Hits to DB: 3738

Number of extensions: 2121

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits) X2: 38 (14.6 bits)

Brast Result Page 1 of 3



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix
BLOSUM62
gap open:
11
gap extension:
1

x_dropoff:
15
expect:
10.000!
wordsize:
3
Filter
✓ View option
Standard

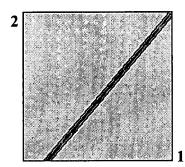
Masking character option
X for protein, n for nucleotide
Masking color option
Black

Show CDS translation
Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $|c||seq_2|$ Length = 639 (1 .. 639)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 1281 bits (3314),Expect = 0.0Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%) SERTONO 122 LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV 17 Sbjct LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV 1 182 WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK Query WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK Sbjct 61 242 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 301 Query DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 180 Sbjct 121 302 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS 361 Query $\verb|HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS|$ 181 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS Sbjct

Blast Result Page 2 of 3

```
362 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                          421
Query
           TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
      241 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                          300
Sbjct
      422 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                          481
Query
           GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
      301 GTALLLKLAOMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                          360
Sbjct
      482 INLDKAVLGTSNFKVSASPLLYTLIEKTMONVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Query
           INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct
      361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
                                                                          420
      542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                          601
Query
           FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
      421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                          480
Sbjct
      602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                          661
Query
           THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
     481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                          540
Sbjct
      662 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
                                                                          721
Query
           NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
      541 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ 600
Sbjct
      722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Query
           NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                    639
Sbjct
      601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                          0.03 total secs.
                                  0.00 sys. secs
CPU time:
             0.03 user secs.
Lambda
          K
  0.318
          0.135
                    0.399
Gapped
Lambda
          K
          0.0410
                    0.140
  0.267
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
```



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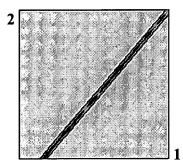
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1	
x_dropoff: 15 expect: 10.000 wordsize: 3 <u>Filter</u> ✓ View option Standard	
Masking character option X for protein, n for nucleotide Masking color option Black	
☐ Show CDS translation Align	

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $|c||seq_2$ Length = 639 (1 .. 639)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



```
Expect = 0.0
         Score = 1281 \text{ bits } (3314),
         Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)
& a I DNO
                   LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV
                    LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
  (8
                                                                                    60
                    LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV
        Sbjct
               1
               182
                   WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
                    WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
        Sbjct
               61
                    WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
                                                                                    120
                    DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
                                                                                    301
        Query
                    DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
                   DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
                                                                                    180
        Sbjct
               121
                                                                                    361
               302 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
                    HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
               181 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
        Sbjct
```

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```
362 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                           421
           TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
      241 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                           300
Sbjct
      422 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                           481
Query
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
      {\tt 301} \quad {\tt GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY}
                                                                           360
Sbjct
      482 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Query
            {\tt INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA}
      361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
                                                                          420
Sbict
      542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Query
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
      421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                          480
Sbjct
      602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Query
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
      481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                          540
Sbjct
      662 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
                                                                           721
Query
           NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
      541 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ 600
Sbjct
      722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Query
           NNGAFNETLFRNOLALATWTIOGAANALSGDVWDIDNEF
      601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                     639
Sbjct
                                                           0.03 total secs.
                                   0.00 sys. secs
CPU time:
           0.03 user secs.
Lambda
          0.135
                     0.399
   0.318
Gapped
Lambda
           K
                     0.140
   0.267
          0.0410
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
```

X2: 38 (14.6 bits)



S NCBI Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

```
Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ✓ View option Standard

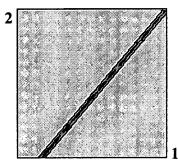
Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align
```

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $|c||seq_2$ Length = 639 (1 .. 639)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



```
Score = 1281 \text{ bits } (3314),
                           Expect = 0.0
 Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)
       122 LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV
            LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
Sbjct
      1
            LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV
                                                                           60
       182 WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
Query
            WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
Sbjct
       61
            WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
                                                                           301
           DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
Query
            DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
                                                                           180
Sbjct
       121 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
                                                                           361
Query
       302 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
            HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
Sbjct
      181 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
```



```
362 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                           421
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
       241 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                          300
Sbjct
      422 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                           481
Query
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
       301 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                          360
Sbjct
       482 INLDKAVLGTSNFKVSASPLLYTLIEKTMONVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Query
            \verb|INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA|
      361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
                                                                          420
Sbjct
      542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Query
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
       421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                          480
Sbjct
       602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                           661
Query
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
      481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                          540
Sbjct
       662 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
                                                                          721
Query
           NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
      541 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct
      722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Query
            NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
      601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                     639
Sbjct
                                    0.01 sys. secs
                                                           0.05 total secs.
CPU time:
              0.04 user secs.
Lambda
          K
          0.135
   0.318
                     0.399
Gapped
Lambda
          K
                 Н
   0.267
           0.0410
                     0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix
BLOSUM62
gap open: 11
gap extension: 1

x_dropoff: 15
expect: 10.000/ wordsize: 3
Filter ✓ View option Standard

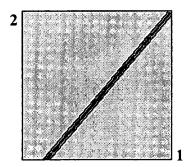
Masking character option
X for protein, n for nucleotide
Masking color option
Black

Show CDS translation
Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $|c||seq_2$ Length = 639 (1 .. 639)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Expect = 0.0Score = 1281 bits (3314),SEQIONO Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%) 122 LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV 181 LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV 20 60 LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV Sbjct 182 WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK Query WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK 120 Sbjct WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA Query DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA Sbjct 121 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 180 361 302 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS Query HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS 181 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS 240 Sbjct

```
TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                          421
Query
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                          300
Sbjct
       241
       422 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                          481
Query
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
       301 GTALLLKLAOMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                          360
Sbjct
       482 INLDKAVLGTSNFKVSASPLLYTLIEKTMONVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Query
            INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct
       361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
                                                                          420
       542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                          601
Query
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
       421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                          480
Sbjct
       602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                          661
Query
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
       481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct
       662 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
                                                                          721
Query
            NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
       541 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct
       722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Ouery
            NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
       601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                     639
Sbjct
                                                           0.03 total secs.
CPU time:
              0.03 user secs.
                                   0.00 sys. secs
Lambda
          K
   0.318
         0.135
                     0.399
Gapped
Lambda
           K
                 Η
   0.267
           0.0410
                     0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
```

11/17/2006

Effective length of database: 1,433,654,247

Number of HSP's gapped: 1

Length of query: 760

X1: 16 (7.3 bits) X2: 38 (14.6 bits)

Length adjustment: 143

Number of HSP's successfully gapped: 1

Effective search space: 884564670399 Effective search space used: 884564670399

Length of database: 1,433,654,390

Effective length of query: 617

Neighboring words threshold: 9



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix
BLOSUM62
gap open:
11
gap extension:
1

x_dropoff:
15
expect:
10.000| wordsize:
3
Filter
✓ View option
Standard

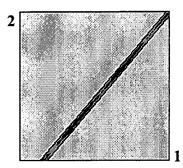
Masking character option
X for protein, n for nucleotide
Masking color option
Black

Show CDS translation
Align

Sequence 1: <u>gi|14720550|ref|XP_052730.1|</u>transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: $|c||seq_2$ Length = 639 (1 .. 639)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1281 bits (3314),Expect = 0.0Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%) SEQIDNO 122 LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV 60 Sbjct 1 LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV 21 182 WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK Sbjct 61 WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK 120 301 Query 242 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 121 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 180 Sbjct 361 Query 302 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS 181 HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS 240 Sbjct

```
362 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                          421
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
Sbjct 241 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
                                                                         300
      422 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                          481
Query
           GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
      301 GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
                                                                         360
Sbjct
      482 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Query
            {\tt INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA}
      361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA 420
Sbjct
      542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Query
           FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
      421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
                                                                         480
Sbjct
      602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                         661
Query
           THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
      481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
                                                                         540
Sbjct
      662 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
                                                                         721
           NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
      541 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ 600
Sbjct
      722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
           NNGAFNETLFRNOLALATWTIOGAANALSGDVWDIDNEF
Sbjct 601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
                                                    639
                                                          0.04 total secs.
                                 0.01 sys. secs
CPU time: 0.03 user secs.
Lambda
         K
  0.318 0.135
                    0.399
Gapped
Lambda
          K
  0.267 0.0410
                    0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
```



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ✓ View option Standard

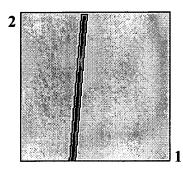
Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: gi|2144140|pir||S68317transferrin receptor - guinea pig (fragment) >gi|1336700|gb|AAB35972.1| transferrin receptor; TfR [Cavia] Length = 63 (1 .. 63)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 118 bits (295), Expect = 2e-24

Identities = 54/63 (85%), Positives = 57/63 (90%), Gaps = 0/63 (0%)

Query 261 KITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHAHLGTGDPYTPGFPSFNHTQ 320 KITFAEKVANAESLNA+GVLIY+D TKFPI A+L FGH HLGTGDPYTPGFPSFNHTQ

22 Sbjct 1 KITFAEKVANAESLNALGVLIYLDWTKFPIPKADLPVFGHVHLGTGDPYTPGFPSFNHTQ 60

Query 321 FPP 323 FPP Sbjct 61 FPP 63

CPU time:

0.03 user secs.

http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?7

Н

0.01 sys. secs

0.04 total secs.

Lambda

K

```
0.318
          0.135 0.399
Gapped
Lambda
           K
           0.0410
                     0.140
   0.267
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 413
Number of extensions: 242
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```





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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

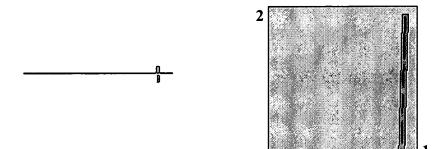
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ✓ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: gi|254113|gb|AAB22984.1|transferrin receptor [human, Peptide Partial, 17 aa] Length = 17 (1 .. 17)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 40.4 bits (93), Expect = 0.60 **SEQIDNO** Identities = 17/17 (100%), Positives = 17/17 (100%), Gaps = 0/17 (0%)

Overy 680 PVEYHELSPYUSPKESP 696

Query 680 RVEYHFLSPYVSPKESP 696 RVEYHFLSPYVSPKESP 2 2 Sbjct 1 RVEYHFLSPYVSPKESP 17

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H 0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

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Matrix: BLOSUM62 Gap Penalties: Existence: 11, Extension: 1 Number of Sequences: 1 Number of Hits to DB: 79 Number of extensions: 46 Number of successful extensions: 1 Number of sequences better than 10.0: 1 Number of HSP's gapped: 1 Number of HSP's successfully gapped: 1 Length of query: 760 Length of database: 1,433,654,390 Length adjustment: 143 Effective length of query: 617 Effective length of database: 1,433,654,247 Effective search space: 884564670399 Effective search space used: 884564670399 Neighboring words threshold: 9 X1: 16 (7.3 bits) X2: 129 (49.7 bits) X3: 129 (49.7 bits) S1: 41 (21.7 bits) S2: 83 (36.6 bits)



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

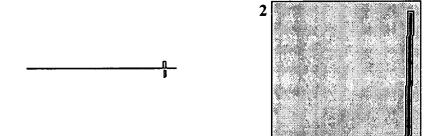
x_dropoff: 50 expect: 10.0001 wordsize: 3 Filter ✓ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: gi|957304|gb|AAB34741.1|transferrin receptor p95, TfR p95 {internal fragment} [human, prostatic-carcinoma cell line DU 145, Peptide Partial, 15 aa, segment 2 of 2] Length = 15 (1 .. 15)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
Score = 38.9 bits (89), Expect = 1.7

Identities = 15/15 (100%), Positives = 15/15 (100%), Gaps = 0/15 (0%)

Query 694 ESPFRHVFWGSGSHT 708

ESPFRHVFWGSGSHT

24 Sbjct 1 ESPFRHVFWGSGSHT 15
```

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda K H 0.318 0.135 0.399

Gapped Lambda K H 0.267 0.0410 0.140

Matrix: BLOSUM62 Gap Penalties: Existence: 11, Extension: 1 Number of Sequences: 1 Number of Hits to DB: 74 Number of extensions: 45 Number of successful extensions: 1 Number of sequences better than 10.0: 1 Number of HSP's gapped: 1 Number of HSP's successfully gapped: 1 Length of query: 760 Length of database: 1,433,654,390 Length adjustment: 143 Effective length of query: 617 Effective length of database: 1,433,654,247 Effective search space: 884564670399 Effective search space used: 884564670399 Neighboring words threshold: 9 X1: 16 (7.3 bits) X2: 129 (49.7 bits) X3: 129 (49.7 bits) S1: 41 (21.7 bits) S2: 83 (36.6 bits)



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

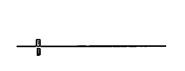
x_dropoff: 100 expect: 10.000 wordsize: 3 Filter ✓ View option Standard

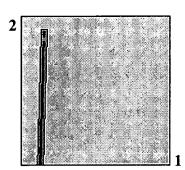
Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: gi|233761|gb|AAB19499.1|transferrin receptor [human, K562 erythroleukemia cells, Peptide Partial, 23 aa] Length = 23 (1 .. 23)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 37.7 bits (86), Expect = 3.9
Identities = 18/22 (81%), Positives = 18/22 (81%), Gaps = 0/22 (0%)

QUETY 101 LAGTESPVREEPGEDFPAARRL 122
LAG ESPV EEP EDFPAA RL

Sbjct 1 LAGKESPVVEEPXEDFPAAXRL 22

CPU time:

0.03 user secs.

0.00 sys. secs

0.03 total secs.

Lambda 0.318

к н 0.135

0.399

Gapped

Lambda

H

K

http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?4

Blast Result Page 2 of 2

0.267 0.0410 0.140

Matrix: BLOSUM62 Gap Penalties: Existence: 11, Extension: 1 Number of Sequences: 1 Number of Hits to DB: 108 Number of extensions: 69 Number of successful extensions: 1 Number of sequences better than 10.0: 1 Number of HSP's gapped: 1 Number of HSP's successfully gapped: 1 Length of query: 760 Length of database: 1,433,654,390 Length adjustment: 143 Effective length of query: 617 Effective length of database: 1,433,654,247 Effective search space: 884564670399 Effective search space used: 884564670399 Neighboring words threshold: 9 X1: 16 (7.3 bits) X2: 259 (99.8 bits) X3: 259 (99.8 bits) S1: 41 (21.7 bits) S2: 83 (36.6 bits)

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 10 gap extension: 2

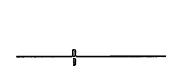
x_dropoff: 200 expect: 10.000 wordsize: 3 Filter ✓ View option Standard

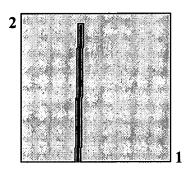
Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: $gi|14720550|ref|XP_052730.1|$ transferrin receptor (p90, CD71) [Homo sapiens] Length = 760 (1 .. 760)

Sequence 2: gi|957302|gb|AAB34739.1|transferrin receptor p95, TfR p95 {internal fragment} [human, prostatic-carcinoma cell line DU 145, Peptide Partial, 15 aa, segment 1 of 2] Length = 15 (1 .. 15)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 38.2 bits (82), Expect = 3.1
Identities = 15/15 (100%), Positives = 15/15 (100%), Gaps = 0/15 (0%)

**CIDNO
Query 288 FPIVNAELSFFGHAH 302
FPIVNAELSFFGHAH

Character Score = 38.2 bits (82), Expect = 3.1

Comparison of the second sec

0.04 user secs.

0.01 sys. secs

0.05 total secs.

Lambda K H 0.318 0.399

Gapped

CPU time:

Lambda K H

Blast Result Page 2 of 2

0.291 0.0750 0.230

Matrix: BLOSUM62 Gap Penalties: Existence: 10, Extension: 2 Number of Sequences: 1 Number of Hits to DB: 77 Number of extensions: 50 Number of successful extensions: 1 Number of sequences better than 10.0: 1 Number of HSP's gapped: 1 Number of HSP's successfully gapped: 1 Length of query: 760 Length of database: 1,433,654,390 Length adjustment: 96 Effective length of query: 664 Effective length of database: 1,433,654,294 Effective search space: 951946451216 Effective search space used: 951946451216 Neighboring words threshold: 9 X1: 16 (7.3 bits) X2: 476 (199.8 bits) X3: 476 (199.8 bits) S1: 41 (21.7 bits) S2: 78 (36.5 bits)

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